



## *Emerging Topics in Biological Networks and Systems Biology*

Symposium at the Swedish Collegium for Advanced Study (SCAS), Uppsala  
9-11 October, 2017

**RICHARD BONNEAU**, New York University, USA

*Methods for Learning Network Models Underlying Immune-microbiome Interactions*

### **Abstract:**

I will discuss our efforts to model diverse immune cell types and their interactions with their environment and with the microbiome. The first part of the talk will detail new efforts to learn large scale biophysically motivated network models of both rare and common immune cell types as they respond to diverse stimuli (including stimuli from microbiome perturbations). Here I will focus on ways of integrating new genomics data-types to constrain network model selection. This inference results in both network models and estimates of regulatory factor activity in a host of conditions. I'll detail our method for learning networks and discuss key challenges that stand in our way as we aim for ever more biologically detailed model descriptions. I'll describe recent efforts to both learn these networks and use the networks to model connections to complex meta-data (such as host immune factors, genetics and metabolites) as well as new methods for making sense of microbiome time series. In the second part of the talk I will discuss methods for predicting the function of large protein families of unknown function found in microbial consortia. We are using machine learning to integrate protein structure prediction, protein networks and genome structure to predict the function and fold of many thousands of new protein families. This work leverages a large scale collaboration with IBM (to fold the many proteins required), for more information see [https://www.ibm.com/blogs/citizen-ibm/2017/08/wcgrid\\_microbiome.html](https://www.ibm.com/blogs/citizen-ibm/2017/08/wcgrid_microbiome.html). The talk will finish with some discussion of limitations and implications for experimental design (alas, most questions posed during the talk will go unanswered).

### **About:**

Dr. Bonneau is Group Leader for Systems Biology at the newly founded Flatiron Institute in New York City and also Director of the New York University Center for Data Science. His group works on inferring and modeling both biological and social networks (at the Simons foundation and the SMaPP lab at NYU respectively), developing new methods to learn very large networks from large collections of genomics data. His group actively participates in applying these methods to ongoing systems biology consortia efforts that span bacteria, model systems, bacteria, the immune system and crop plants. His group also develops methods for the prediction and design of bio molecular polymers (and polymers that mimic biological structure). To carry out this work his group develops Rosetta as a core member of the RosettaCommons; Dr. Bonneau is a founding member of the Rosetta commons and a member of the RosettaCommons executive board. Dr. Bonneau is committed to doing all he can to leverage his position as Director of the Center for Data Science to help increase diversity in the many computational fields that comprise what we today refer to as the field of data science.